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RAW SEQUENCE LISTING

DATE: 11/06/2002

PATENT APPLICATION: US/09/741,843A

TIME: 10:23:51

Input Set : A:\Leung.txt

Output Set: N:\CRF4\11062002\I741843A.raw

4 <110> APPLICANT: LEUNG, Shui-on
5 HANSEN, Hans
7 <120> TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
8 LYMPHOMA AND LEUKEMIA CELLS
10 <130> FILE REFERENCE: 018733/0996
12 <140> CURRENT APPLICATION NUMBER: US 09/741,843A
13 <141> CURRENT FILING DATE: 2000-12-22
15 <150> PRIOR APPLICATION NUMBER: US 09/127,902
16 <151> PRIOR FILING DATE: 1998-08-03
18 <150> PRIOR APPLICATION NUMBER: US 08/690,102
19 <151> PRIOR FILING DATE: 1996-07-06
21 <150> PRIOR APPLICATION NUMBER: US 08/289,576
22 <151> PRIOR FILING DATE: 1994-08-12
24 <160> NUMBER OF SEQ ID NOS: 25
26 <170> SOFTWARE: PatentIn version 3.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 339
30 <212> TYPE: DNA
31 <213> ORGANISM: Murinae gen. sp.
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)..(339)
36 <223> OTHER INFORMATION:
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39 gac att cag ctg acc cag tct cca tca tct ctg gct gtg tct gca gga 48
40 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
41 1 5 10 15
43 gaa aac gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96
44 Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
45 20 25 30
47 gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag 144
48 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
49 35 40 45
51 tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192
52 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
53 50 55 60
55 cct gat cgc ttc aca ggc agc gga tct ggg aca gat ttt act ctt acc 240
56 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
57 65 70 75 80
59 atc agc aga gta caa gtt gaa gac ctg gca att tat tat tgt cac caa 288
60 Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
61 85 90 95
63 tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag ctg gag atc aaa 336

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64 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 65 100 105 110

67 cgt

339

68 Arg

72 <210> SEQ ID NO: 2

73 <211> LENGTH: 113

74 <212> TYPE: PRT

75 <213> ORGANISM: Murinae gen. sp.

77 <400> SEQUENCE: 2

78 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly

79 1 5 10 15

82 Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser

83 20 25 30

86 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

87 35 40 45

90 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val

91 50 55 60

94 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

95 65 70 75 80

98 Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln

99 85 90 95

102 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

103 100 105 110

106 Arg

110 <210> SEQ ID NO: 3

111 <211> LENGTH: 348

112 <212> TYPE: DNA

113 <213> ORGANISM: Murinae gen. sp.

115 <220> FEATURE:

116 <221> NAME/KEY: CDS

117 <222> LOCATION: (1)..(348)

118 <223> OTHER INFORMATION:

W--> 120 <400> 3

121 cag gtc cag ctg cag gag tca ggg gct gaa ctg tca aaa cct ggg gcc 48

122 Gln Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ser Lys Pro Gly Ala

123 1 5 10 15

125 tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt act agc tac 96

126 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

127 20 25 30

129 tgg ctg cac tgg ata aaa cag agg cct gga cag ggt ctg gaa tgg att 144

130 Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

131 35 40 45

133 gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc 192

134 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe

135 50 55 60

137 aag gac aag gcc aca ttg act gca gac aaa tcc tcc agc aca gcc tac 240

138 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

139 65 70 75 80

141 atg caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt 288

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Input Set : A:\Leung.txt

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142 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
143           85           90           95
145 gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc act ctc      336
146 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
147           100           105           110
149 aca gtc tcc tcg      348
150 Thr Val Ser Ser
151           115
154 <210> SEQ ID NO: 4
155 <211> LENGTH: 116
156 <212> TYPE: PRT
157 <213> ORGANISM: Murinae.gen. sp.
159 <400> SEQUENCE: 4
160 Gln Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ser Lys Pro Gly Ala
161 1           5           10           15
164 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165           20           25           30
168 Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
169           35           40           45
172 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
173           50           55           60
176 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
177 65           70           75           80
180 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
181           85           90           95
184 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
185           100           105           110
188 Thr Val Ser Ser
189           115
192 <210> SEQ ID NO: 5
193 <211> LENGTH: 339
194 <212> TYPE: DNA
195 <213> ORGANISM: Homo sapiens
197 <220> FEATURE:
198 <221> NAME/KEY: CDS
199 <222> LOCATION: (1)..(339)
200 <223> OTHER INFORMATION:
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203 gac att cag ctg acc cag tct cca tca tct ctg agc gca tct gtt gga      48
204 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
205 1           5           10           15
207 gat agg gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt      96
208 Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
209           20           25           30
211 gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg aaa      144
212 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
213           35           40           45
215 gca cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc      192
216 Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val

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217      50      55      60
219 cct tcg cga ttc tct ggc agc gga tct ggg aca gat ttt act ttc acc      240
220 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
221 65      70      75      80
223 atc agc tct ctt caa cca gaa gac att gca aca tat tat tgt cac caa      288
224 Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
225      85      90      95
227 tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag gtg cag atc aaa      336
228 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Thr Lys Val Gln Ile Lys
229      100      105      110
231 cgt      339
232 Arg
236 <210> SEQ ID NO: 6
237 <211> LENGTH: 113
238 <212> TYPE: PRT
239 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 6
242 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
243 1      5      10      15
246 Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
247      20      25      30
250 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
251      35      40      45
254 Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
255      50      55      60
258 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
259 65      70      75      80
262 Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
263      85      90      95
266 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys
267      100      105      110
270 Arg
273 <210> SEQ ID NO: 7
274 <211> LENGTH: 348
275 <212> TYPE: DNA
276 <213> ORGANISM: Homo sapiens
278 <220> FEATURE:
279 <221> NAME/KEY: CDS
280 <222> LOCATION: (1)..(348)
281 <223> OTHER INFORMATION:
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284 cag gtc cag ctg gtc caa tca ggg gct gaa gtc aag aaa cct ggg tca      48
285 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
286 1      5      10      15
288 tca gtg aag gtc tcc tgc aag gct tct ggc tac acc ttt act agc tac      96
289 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
290      20      25      30
292 tgg ctg cac tgg gtc agg cag gca cct gga cag ggt ctg gaa tgg att      144
293 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

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294          35          40          45
296 gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc      192
297 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
298          50          55          60
300 aag gac aag gcc aca ata act gca gac gaa tcc acc aat aca gcc tac      240
301 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
302 65          70          75          80
304 atg gag ctg agc agc ctg agg tct gag gac acg gca ttt tat ttt tgt      288
305 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
306          85          90          95
308 gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc acg gtc      336
309 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
310          100          105          110
312 acc gtc tcc tcg      348
313 Thr Val Ser Ser
314          115
317 <210> SEQ ID NO: 8
318 <211> LENGTH: 116
319 <212> TYPE: PRT
320 <213> ORGANISM: Homo sapiens
322 <400> SEQUENCE: 8
323 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
324 1          5          10          15
327 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
328          20          25          30
331 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
332          35          40          45
335 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
336          50          55          60
339 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
340 65          70          75          80
343 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
344          85          90          95
347 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
348          100          105          110
351 Thr Val Ser Ser
352          115
355 <210> SEQ ID NO: 9
356 <211> LENGTH: 116
357 <212> TYPE: PRT
358 <213> ORGANISM: Homo sapiens
360 <400> SEQUENCE: 9
361 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
362 1          5          10          15
365 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
366          20          25          30
369 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
370          35          40          45
373 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe

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VERIFICATION SUMMARY

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TIME: 10:23:52

Input Set : A:\Leung.txt

Output Set: N:\CRF4\11062002\I741843A.raw

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L:120 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:118
L:202 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:200
L:283 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:281
L:563 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:561
L:587 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:585
L:611 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:609
L:635 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:633